BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

図 1

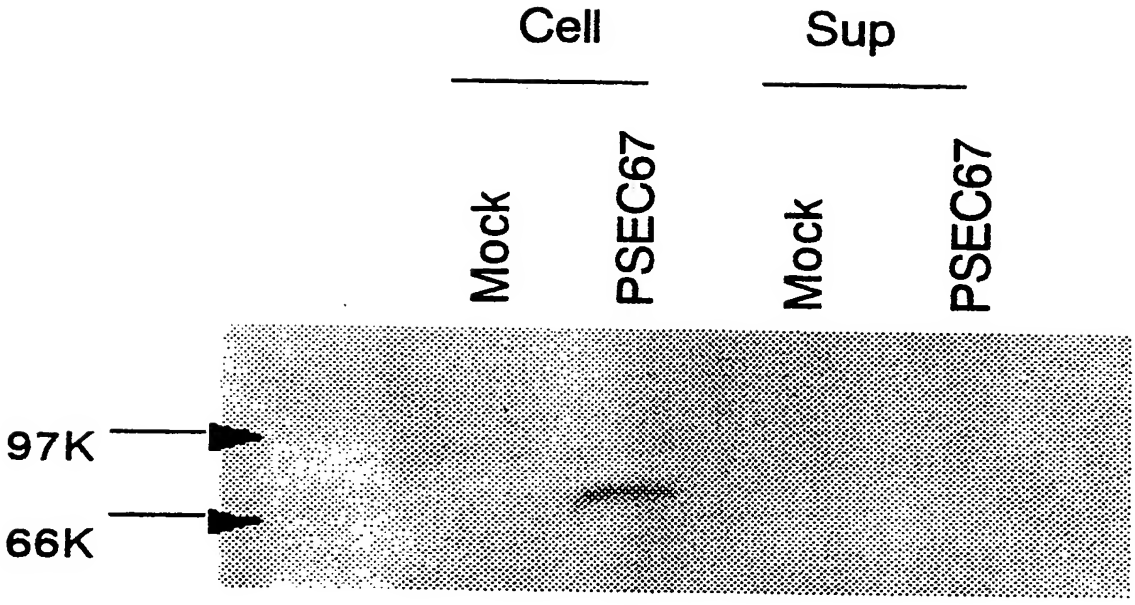


図2

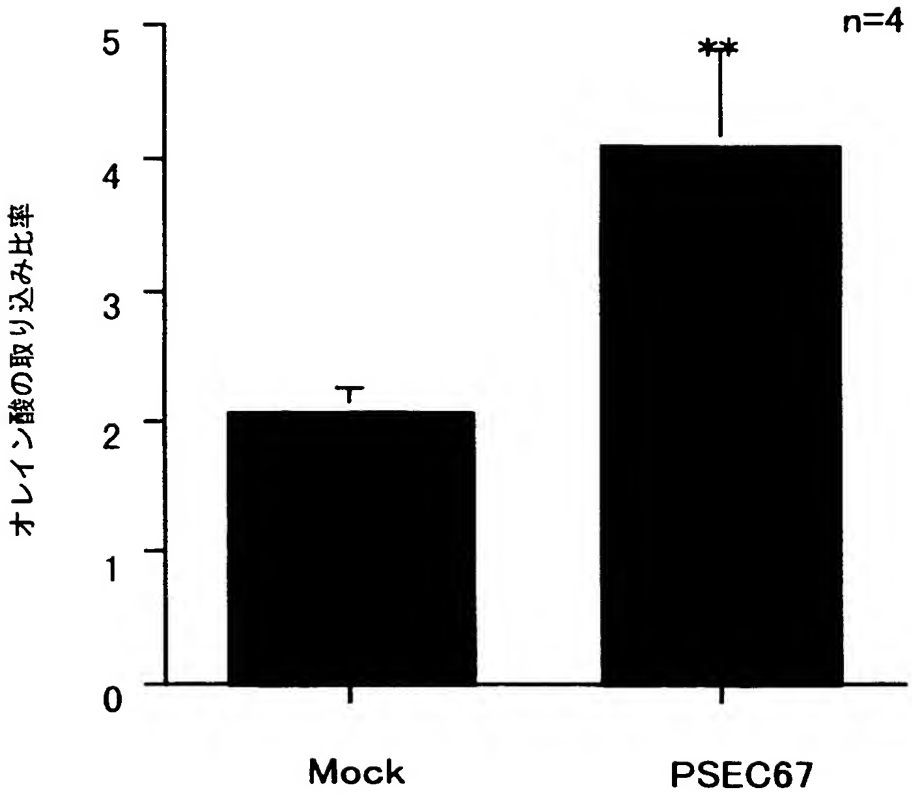


図3

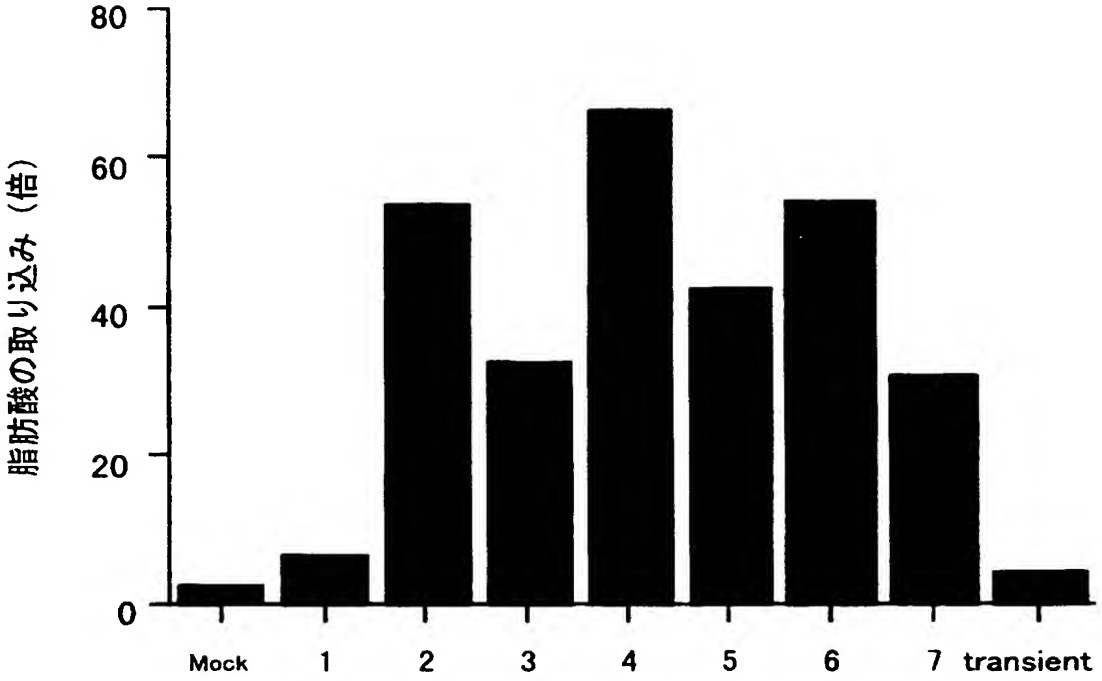


図4

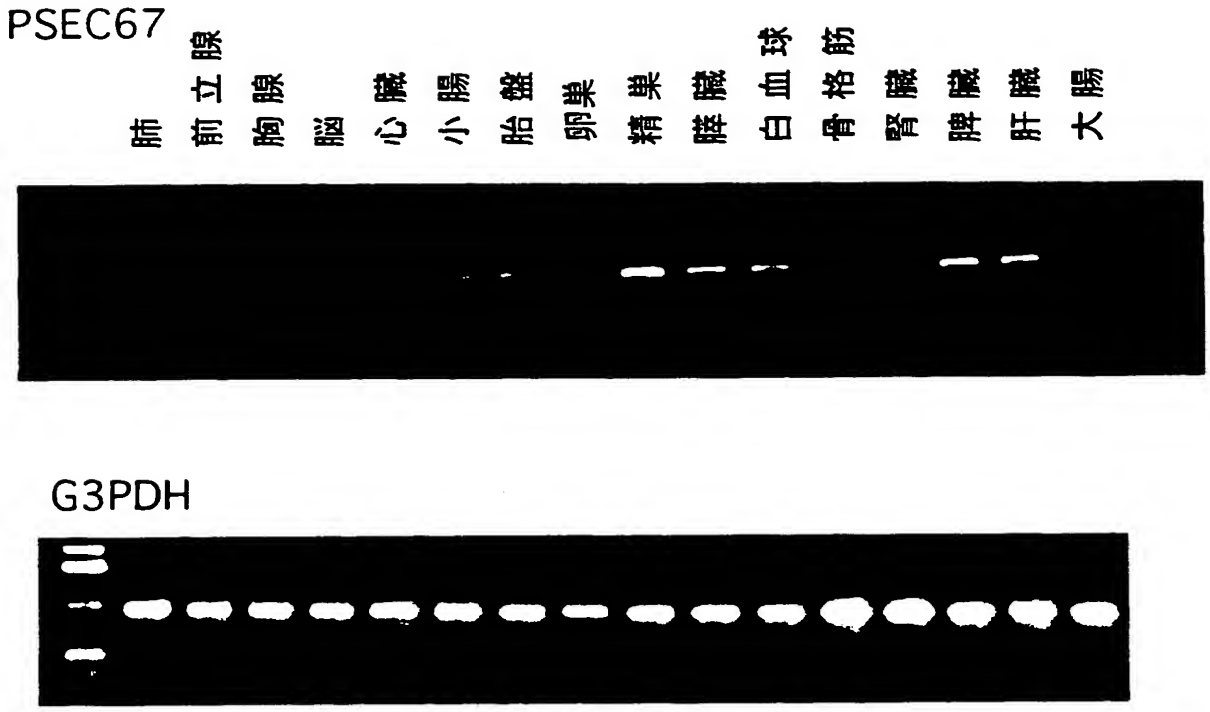


図5

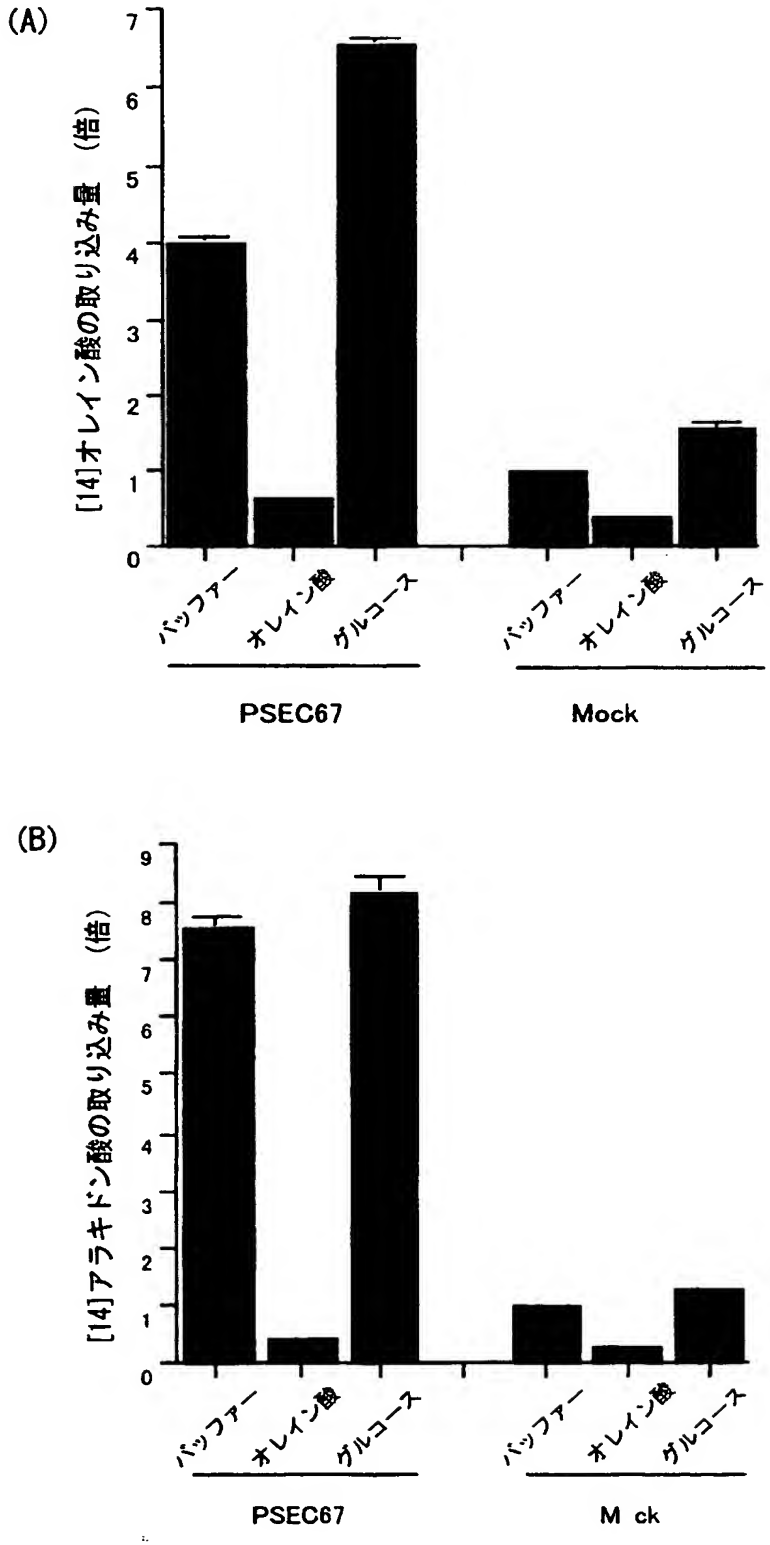

(A)
[14]オレイン酸の取り込み量 (倍)
0
1
2
3
4
5
6
7
バッファー
オレイン酸
グルコース
バッファー
オレイン酸
グルコース
PSEC67
Mock
(B)
[14]アラキドン酸の取り込み量 (倍)
0
1
2
3
4
5
6
7
8
9
バッファー
オレイン酸
グルコース
バッファー
オレイン酸
グルコース
PSEC67
M ck

図6

```
PSEC67:  501 ACAGGGCTGCACGCGCCTTC-CTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCG-G 558
             AC G GC GCA GCGC TT  CTACG G G  AGGCTG G C  G GA C   CGG   G
m.FATP3:  98 ACGGCGC-GCA-GCGCTTTAGCTACGCG-G--AGGCTGAG-CGCGAGAGCAACCGGATTG 151

PSEC67:  559 CGACAGCGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCG-GGAGCCGG-AGAT 616
             C  C GCG C     G GCGC  G G   G GA CGGG   CGCCG GG  C GG AG
m.FATP3: 152 CT-C-GCGCCTTTCTGCGCGCACGGGGCTG-GACCGGGGGCCGCCGAGGCTCGGGCAGGG 208

PSEC67:  617 GCAGCGGCC-GGAAG-CGG-CGCG--GAGTTTGCCGGAGGG-GACGGTGCCGCCAGAGGT 670
             GCAGC     GGAAG CG  CGCG  G G  T CCGG  GG GA G  GC GC AGAGG
m.FATP3: 209 GCAGCACTGAGGAAGGCGCACGCGTGGCGCCT-CCGGCTGGAGATGCGGCTGCTAGAGG- 266

PSEC67:  671 GGAGGAGCCGCCGCCCCTCTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGC 730
              GA GA CCGC  CCCCTCTG CACC GG GC AC GTGGCGCTGCTCCTCCC GC GGC
m.FATP3: 267 -GACGA-CCGCGCCCCCTCTGGCACCCGGGGCGACCGTGGCGCTGCTCCTCCCAGCGGGC 324

PSEC67:  731 CCAGAGTTTCTGTGGCTCTGGTTCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTG 790
             CC GA TT CT TGG T TGGTTCGG CTGGCCAA GC GGCCTGCGCAC GCCTTTGTG
m.FATP3: 325 CCGGATTTCCTTTGGATTTGGTTCGGACTGGCCAAAGCTGGCCTGCGCACGGCCTTTGTG 384

PSEC67:  791 CCCACCGCCCTGCGCCGGGGCCCCCTGCTGCACTGCCTCCGCAGCTGCGGCGCGCGCGCG 850
             CCCACCGC  T CGCCG GG CCCCTGCTGCACTGCCTCCGCAGCTGCGG GCG G GCG
m.FATP3: 385 CCCACCGCTTTACGCCGAGGACCCCTGCTGCACTGCCTCCGCAGCTGCGGTGCGAGTGCG 444

PSEC67:  851 CTGGTGCTGGCGCCAGAGTTTCTGGAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCC 910
             CT GTGCTGGC  CAGAGTT CTGGAGTCCCTGGAGCCGGACCTGCC GCC TGAGAGCC
m.FATP3: 445 CTCGTGCTGGCCACAGAGTTCCTGGAGTCCCTGGAGCCGGACCTGCCGGCCTTGAGAGCC 504

PSEC67:  911 ATGGGGCTCCACCTGTGGGCTGCAGGCCCAGGAACCCACCCTGCTGGAATTAGCGATTTG 970
             ATGGGGCTCCACCT TGGGC  C GGCCC G AAC  A    GCTGGAAT AGC ATTTG
m.FATP3: 505 ATGGGGCTCCACCTATGGGCGACGGGCCCTGAAACTAATGTAGCTGGAATCAGCAATTTG 564

PSEC67:  971 CTGGCTGAAGTGTCCGCTGAAGTGGATGGGCCAGTGCCAGGATACCTCTCTTCCCCCCAG 1030
             CT  C GAAG   C G   AAGTGGATG GCCAGTGCC GG TACCTCTCT CCCCCCAG
m.FATP3: 565 CTATCGGAAGCAGCAGACCAAGTGGATGAGCCAGTGCCGGGGTACCTCTCTGCCCCCCAG 624

PSEC67: 1031 AGCATAACAGACACGTGCCTGTACATCTTCACCTCTGGCACCACGGGCCTCCCCAAGGCT 1090
             A CATAA  GACAC TGCCTGTACATCTTCACCTCTGGCAC AC GGCCT CCCAAGGCT
m.FATP3: 625 AACATAATGGACACCTGCCTGTACATCTTCACCTCTGGCACTACTGGCCTGCCCAAGGCT 684

PSEC67: 1091 GCTCGGATCAGTCATCTGAAGATCCTGCAATGCCAGGGCTTCTATCAGCTGTGTGGTGTC 1150
             GCTCG ATCAGTCATCTGAAG T CT CA TGCCAGGG TTCTA CA CTGTGTGG GTC
m.FATP3: 685 GCTCGAATCAGTCATCTGAAGGTTCTACAGTGCCAGGGATTCTACCATCTGTGTGGAGTC 744

PSEC67: 1151 CACCAGGAAGATGTGATCTACCTCGCCCTCCCACTCTACCACATGTCCGGTTCCCTGCTG 1210
             CACCAGGA GA GTGATCTACCTCGC CTCCCACT TACCACATGTC GG TCCCT CTG
m.FATP3: 745 CACCAGGAGGACGTGATCTACCTCGCACTCCCACTGTACCACATGTCTGGCTCCCTTCTG 804

PSEC67: 1211 GGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTGGTGCTGAAATCCAAGTTCTCGGCT 1270
             GGCAT GTGGGCTGC TGGGCATTGGGGCCAC GTGGTGCTGAAA CCAAGTTCTC GCT
m.FATP3: 805 GGCATTGTGGGCTGCTTGGGCATTGGGGCCACCGTGGTGCTGAAACCCAAGTTCTCAGCT 864
```

図7

```
PSEC67: 1271 GGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGACGGTGTTCCAGTACATTGGGGAG 1330
             G CAGTTCTGGGA GATTGCCAG A CACAGGGTGAC GTGTTCCAGTACATTGGGGAG
m.FATP3: 865 AGCCAGTTCTGGGACGATTGCCAGAAACACAGGGTGACAGTGTTCCAGTACATTGGGGAG 924

PSEC67: 1331 CTGTGCCGATACCTTGTCAACCAGCCCCCGAGCAAGGCAGAACGTGGCCATAAGGTCCGG 1390
             TGTGCCGATACCT GTCAACCAGCCCCCGAGCAAGGCAGA  TG CCATAAGGT CG
m.FATP3: 925 TTGTGCCGATACCTCGTCAACCAGCCCCCGAGCAAGGCAGAGTTTGACCATAAGGTGCGC 984

PSEC67: 1391 CTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGTTTTGTGCGGCGCTTCGGG 1450
             TGGCAGTGGGCAG GGG TGCGCCCAGA ACCTGGGAGCGTTT  TGCGGCG TT GG
m.FATP3: 985 TTGGCAGTGGGCAGTGGGTTGCGCCCAGACACCTGGGAGCGTTTCCTGCGGCGATTTGGA 1044

PSEC67: 1451 CCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGTGGCCACCATCAACTAC 1510
             CC CTGCAG T CTGGAGAC TATGG  TGACAGAGGGCAACGT GC AC  TCAA TAC
m.FATP3:1045 CCTCTGCAGATACTGGAGACGTATGGCATGACAGAGGGCAACGTAGCTACGTTCAATTAC 1104

PSEC67: 1511 ACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGCATATCTTCCCCTTC 1570
             ACAGGAC GC GGG GC GTGGGGCG GCTTCCTGGCTTTACAAGCA ATCTTCCCCTTC
m.FATP3:1105 ACAGGACGGCAGGGTGCAGTGGGGCGAGCTTCCTGGCTTTACAAGCACATCTTCCCCTTC 1164

PSEC67: 1571 TCCTTGATTCGCTATGATGTCACCACAGGAGAGCCAATTCGGGACCCCCAGGGGCACTGT 1630
             TCCTTGATTCG TA GATGTCA  ACAGG GAGCC ATTCGG A  CCCAGGGGCACTG
m.FATP3:1165 TCCTTGATTCGATACGATGTCATGACAGGGGAGCCTATTCGGAATGCCCAGGGGCACTGC 1224

PSEC67: 1631 ATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCAGCAGTCCCCA 1690
             ATG CCACATCTCCAGGTGAGCCAGG CT CTGGTGGCCCC GT AGCCAGCAGTCCCC
m.FATP3:1225 ATGACCACATCTCCAGGTGAGCCAGGCCTACTGGTGGCCCCAGTGAGCCAGCAGTCCCCC 1284

PSEC67: 1691 TTCCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGGATGTCTTC 1750
             TTCCTGGGCTATGCTGG G  CC GAGCTGGCC AGG  AAG TGCT AAGGATGTCTTC
m.FATP3:1285 TTCCTGGGCTATGCTGGGGCTCCGGAGCTGGCCAAGGACAAGCTGCTGAAGGATGTCTTC 1344

PSEC67: 1751 CGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAAGGTTTT 1810
              GG CTGGGGA GTTTTCTTCAA ACTGGGGACCT  TGGTCTG GATGA CAAGG TTT
m.FATP3:1345 TGGTCTGGGGACGTTTTCTTCAATACTGGGGACCTCTTGGTCTGTGATGAGCAAGGCTTT 1404

PSEC67: 1811 CTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGCCACA 1870
             CT C CTTCCA GATCGTACTGGAGACACC TCAGGTGGAAGGG GAGAATGTGGCCACA
m.FATP3:1405 CTTCACTTCCACGATCGTACTGGAGACACCATCAGGTGGAAGGGAGAGAATGTGGCCACA 1464

PSEC67: 1871 ACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATGGA 1930
             AC GA GTGGC GAGGTCTT GAG CCCT GA TT CTTCAGGAGGTGAAC TCTATGGA
m.FATP3:1465 ACTGAAGTGGCTGAGGTCTTGGAGACCCTGGACTTCCTTCAGGAGGTGAACATCTATGGA 1524

PSEC67: 1931 GTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCCC 1990
             GTCAC GTGCCAGGGCA GAAGGCAGGGC GG ATGGC GCC T G TCTGCG CCCCC
m.FATP3:1525 GTCACGGTGCCAGGGCACGAAGGCAGGGCAGGCATGGCGGCCTTGGCTCTGCGGCCCCCG 1584

PSEC67: 1991 CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCC 2050
             CA GCT TG ACCT  TGCAGCTCTACA CCA GT TCTGAGAACTTGCCACC TATGCC
m.FATP3:1585 CAGGCTCTGAACCTGGTGCAGCTCTACAGCCATGTTTCTGAGAACTTGCCACCGTATGCC 1644

PSEC67: 2051 CGGCCCCGATTCCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAG 2110
             CG CC CG TT CTCAGGCTCCAGGA TCTTTGGCCAC AC GAGACCTTCAAACAGCAG
m.FATP3:1645 CGACCTCGGTTTCTCAGGCTCCAGGAATCTTTGGCCACTACTGAGACCTTCAAACAGCAG 1704
```

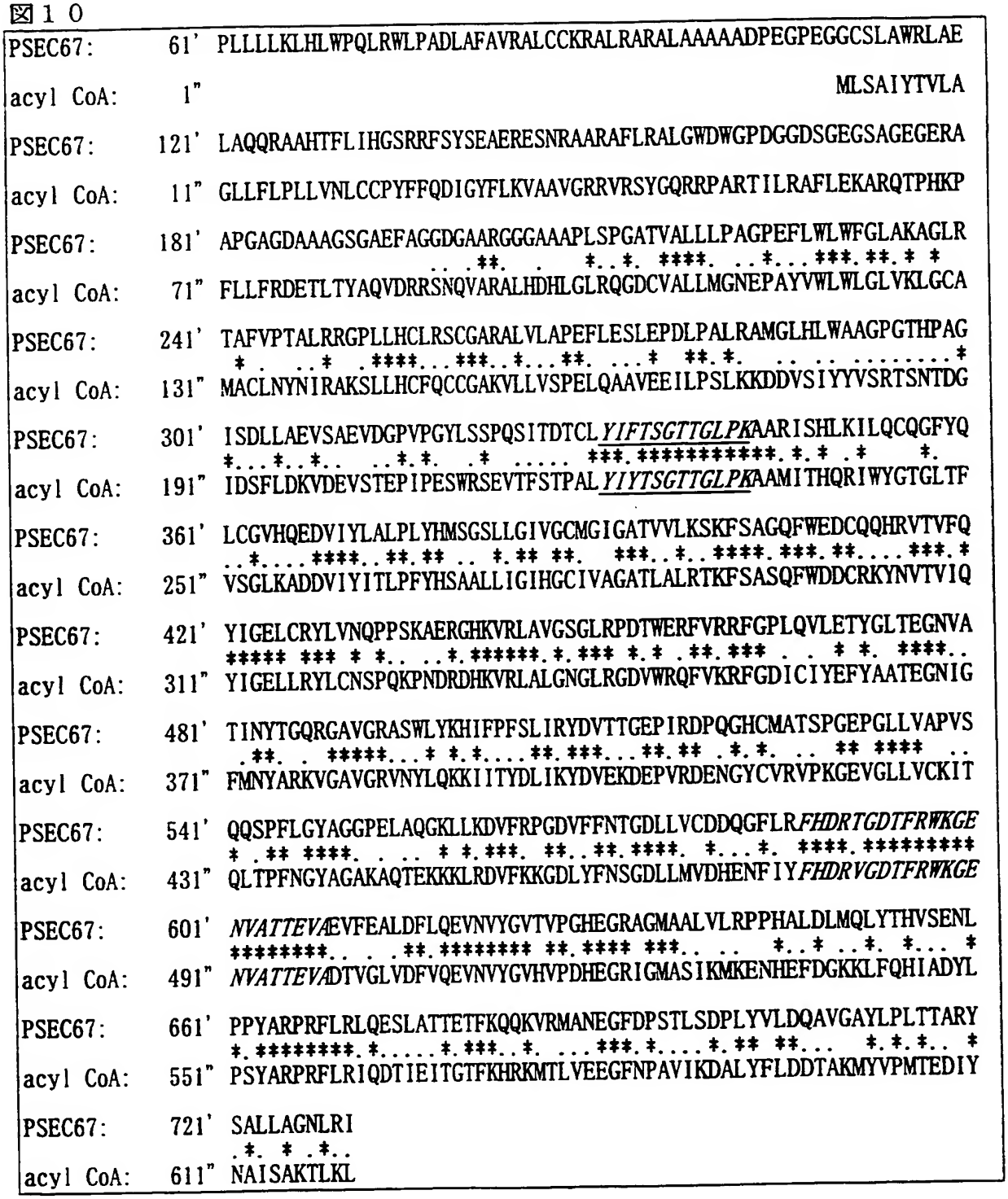
図8

```
PSEC67: 2111 AAAGTTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCCTGTCTGACCCACTGTACGTT 2170
             AA GTT GGATGGC AATGAGGGCTT GACCCCAG     CTGTCTGACCCACT TA GTT
m.FATP3:1705 AAGGTTAGGATGGCCAATGAGGGCTTTGACCCCAGTGTACTGTCTGACCCACTCTATGTT 1764

PSEC67: 2171 CTGGACCAGGCTGTAGGTGCCTACCTGCCCCTCACAACTGCCCGGTACAGCGCCCTCCTG 2230
             CTGGACCA G T TAGG GCCTACCTGCCCCTCACA CTGCCCGGTACAG GCCCTCCTG
m.FATP3:1765 CTGGACCAAGATATAGGGGCCTACCTGCCCCTCACACCTGCCCGGTACAGTGCCCTCCTG 1824

PSEC67: 2231 GCAGGAAACCTTCGAATCTGA 2251
              C GGA ACCTTCGAATCTGA
m.FATP3:1825 TCTGGAGACCTTCGAATCTGA 1845
```

図9

```
PSEC67:      61' PLLLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE
                                                      ******..*.*********
m.FATP3:      1"                                      AAADPESSESGCSLAWRLAY

PSEC67:     121' LAQQRAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERA
                 **.....*******..****.******** ******* **. *. *...  **..**.*.
m.FATP3:     21" LAREQPTHTFLIHGAQRFSYAEAERESNRIARAFLRARGWTGGRRGSGR—GSTEEGARV

PSEC67:     181' APGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLR
                 ** ***              .*** *..*.**.*************.***.**********
m.FATP3:     79" APPAGD————————————AAAR-GTTAPPLAPGATVALLLPAGPDFLWIWFGLAKAGLR

PSEC67:     241' TAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG
                 **********************.*****.**********************.**.*. **
m.FATP3:    125" TAFVPTALRRGPLLHCLRSCGASALVLATEFLESLEPDLPALRAMGLHLWATGPETNVAG

PSEC67:     301' ISDLLAEVSAEVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQ
                 **.**.*....**.*******.**.* ************************.*******.
m.FATP3:    185" ISNLLSEAADQVDEPVPGYLSAPQNIMDTCLYIFTSGTTGLPKAARISHLKVLQCQGFYH

PSEC67:     361' LCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQ
                 ****************************.*********.****.***.***.********
m.FATP3:    245" LCGVHQEDVIYLALPLYHMSGSLLGIVGCLGIGATVVLKPKFSASQFWDDCQKHRVTVFQ

PSEC67:     421' YIGELCRYLVNQPPSKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVA
                 ****************** .*******************.*******.*****.******
m.FATP3:    305" YIGELCRYLVNQPPSKAEFDHKVRLAVGSGLRPDTWERFLRRFGPLQILETYGMTEGNVA

PSEC67:     481' TINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVS
                 *.****..************************ ******..*****.**************
m.FATP3:    365" TFNYTGRQGAVGRASWLYKHIFPFSLIRYDVMTGEPIRNAQGHCMTTSPGEPGLLVAPVS

PSEC67:     541' QQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLRFHDRTGDTFRWKGE
                 **********.****..*******..**************.****.********.*****
m.FATP3:    425" QQSPFLGYAGAPELAKDKLLKDVFWSGDVFFNTGDLLVCDEQGFLHFHDRTGDTIRWKGE

PSEC67:     601' NVATTEVAEVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENL
                 **********.*.********.******************.****.**.*.***.******
m.FATP3:    485" NVATTEVAEVLETLDFLQEVNIYGVTVPGHEGRAGMAALALRPPQALNLVQLYSHVSENL

PSEC67:     661' PPYARPRFLRLQESLATTETFKQQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARY
                 ************************************.**********..*******.***
m.FATP3:    545" PPYARPRFLRLQESLATTETFKQQKVRMANEGFDPSVLSDPLYVLDQDIGAYLPLTPARY

PSEC67:     721' SALLAGNLRI
                 ****.*.***
m.FATP3:    605" SALLSGDLRI
```

図10


PSEC67: 61' PLLLLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGGCSLAWRLAE
acyl CoA: 1" MLSAIYTVLA
PSEC67: 121' LAQQRAAHTFLIHGSRRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERA
acyl CoA: 11" GLLFLPLLVNLCCPYFFQDIGYFLKVAAVGRRVRSYGQRRPARTILRAFLEKARQTPHKP
PSEC67: 181' APGAGDAAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGLAKAGLR
acyl CoA: 71" FLLFRDETLTYAQVDRRSNQVARALHDHLGLRQGDCVALLMGNEPAYVWLWLGLVKLGCA
PSEC67: 241' TAFVPTALRRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAG
acyl CoA: 131" MACLNYNIRAKSLLHCFQCCGAKVLLVSPELQAAVEEILPSLKKDDVSIYYVSRTSNTDG
PSEC67: 301' ISDLLAEVSAEVDGPVPGYLSSPQSITDTCL*YIFTSGTTGLPK*AARISHLKILQCQGFYQ
acyl CoA: 191" IDSFLDKVDEVSTEPIPESWRSEVTFSTPAL*YIYTSGTTGLPK*AAMITHQRIWYGTGLTF
PSEC67: 361' LCGVHQEDVIYLALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQ
acyl CoA: 251" VSGLKADDVIYITLPFYHSAALLIGIHGCIVAGATLALRTKFSASQFWDDCRKYNVTVIQ
PSEC67: 421' YIGELCRYLVNQPPSKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVA
acyl CoA: 311" YIGELLRYLCNSPQKPNDRDHKVRLALGNGLRGDVWRQFVKRFGDICIYEFYAATEGNIG
PSEC67: 481' TINYTGQRGAVGRASWLYKHIFPFSLIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVS
acyl CoA: 371" FMNYARKVGAVGRVNYLQKKIITYDLIKYDVEKDEPVRDENGYCVRVPKGEVGLLVCKIT
PSEC67: 541' QQSPFLGYAGGPELAQGKLLKDVFRPGDVFFNTGDLLVCDDQGFLR*FHDRTGDTFRWKGE
acyl CoA: 431" QLTPFNGYAGAKAQTEKKKLRDVFKKGDLYFNSGDLLMVDHENFIY*FHDRVGDTFRWKGE
PSEC67: 601' *NVATTEVA*EVFEALDFLQEVNVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENL
acyl CoA: 491" *NVATTEVA*DTVGLVDFVQEVNVYGVHVPDHEGRIGMASIKMKENHEFDGKKLFQHIADYL
PSEC67: 661' PPYARPRFLRLQESLATTETFKQQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARY
acyl CoA: 551" PSYARPRFLRIQDTIEITGTFKHRKMTLVEEGFNPAVIKDALYFLDDTAKMYVPMTEDIY
PSEC67: 721' SALLAGNLRI
acyl CoA: 611" NAISAKTLKL

SEQUENCE LISTING

<110> Helix Research Institute

<120> Fatty Acid Transfer Protein, and a gene encoding the protein.

<130> H1-106DP3PCT

<140>
<141>

<150> JP 1999-194179
<151> 1999-07-08

<150> JP 2000-128993
<151> 2000-04-25

<150> US 60/159586
<151> 1999-10-18

<160> 12

<170> PatentIn Ver. 2.0

<210> 1
<211> 2405
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (59)..(2248)

<400> 1
gcactcctcc cgggtttctg ctctccgccc gtgtggagtg gtgggggcct gggtggga 58

atg ggc gtg tgc cag cgc acg cgc gct ccc tgg aag gag aag tct cag 106
Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser Gln
1 5 10 15

cta gaa cga gcg gcc cta ggt ttt cgg aag gga gga tca ggg atg ttt 154
Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly Met Phe
20 25 30

gcg agc ggc tgg aac cag acg gtg ccg ata gag gaa gcg ggc tcc atg 202
Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala Gly Ser Met
35 40 45

```
gct gcc ctc ctg ctg ctg ccc ctg ctg ctg ttg cta ccg ctg ctg ctg   250
Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Pro Leu Leu Leu
     50                  55                  60

ctg aag cta cac ctc tgg ccg cag ttg cgc tgg ctt ccg gcg gac ttg   298
Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp Leu Pro Ala Asp Leu
 65                  70                  75                  80

gcc ttt gcg gtg cga gct ctg tgc tgc aaa agg gct ctt cga gct cgc   346
Ala Phe Ala Val Arg Ala Leu Cys Cys Lys Arg Ala Leu Arg Ala Arg
                 85                  90                  95

gcc ctg gcc gcg gct gcc gcc gac ccg gaa ggt ccc gag ggg ggc tgc   394
Ala Leu Ala Ala Ala Ala Ala Asp Pro Glu Gly Pro Glu Gly Gly Cys
            100                 105                 110

agc ctg gcc tgg cgc ctc gcg gaa ctg gcc cag cag cgc gcc gcg cac   442
Ser Leu Ala Trp Arg Leu Ala Glu Leu Ala Gln Gln Arg Ala Ala His
        115                 120                 125

acc ttt ctc att cac ggc tcg cgg cgc ttt agc tac tca gag gcg gag   490
Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu
    130                 135                 140

cgc gag agt aac agg gct gca cgc gcc ttc cta cgt gcg cta ggc tgg   538
Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp
145                 150                 155                 160

gac tgg gga ccc gac ggc ggc gac agc ggc gag ggg agc gct gga gaa   586
Asp Trp Gly Pro Asp Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu
                165                 170                 175

ggc gag cgg gca gcg ccg gga gcc gga gat gca gcg gcc gga agc ggc   634
Gly Glu Arg Ala Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly
            180                 185                 190

gcg gag ttt gcc gga ggg gac ggt gcc gcc aga ggt gga gga gcc gcc   682
Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala
        195                 200                 205

gcc cct ctg tca cct gga gca act gtg gcg ctg ctc ctc ccc gct ggc   730
Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly
    210                 215                 220

cca gag ttt ctg tgg ctc tgg ttc ggg ctg gcc aag gcc ggc ctg cgc   778
Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg
225                 230                 235                 240
```

```
act gcc ttt gtg ccc acc gcc ctg cgc cgg ggc ccc ctg ctg cac tgc   826
Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys
                245                 250                 255

ctc cgc agc tgc ggc gcg cgc gcg ctg gtg ctg gcg cca gag ttt ctg   874
Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu
            260                 265                 270

gag tcc ctg gag ccg gac ctg ccc gcc ctg aga gcc atg ggg ctc cac   922
Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His
        275                 280                 285

ctg tgg gct gca ggc cca gga acc cac cct gct gga att agc gat ttg   970
Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu
    290                 295                 300

ctg gct gaa gtg tcc gct gaa gtg gat ggg cca gtg cca gga tac ctc   1018
Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu
305                 310                 315                 320

tct tcc ccc cag agc ata aca gac acg tgc ctg tac atc ttc acc tct   1066
Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser
                325                 330                 335

ggc acc acg ggc ctc ccc aag gct gct cgg atc agt cat ctg aag atc   1114
Gly Thr Thr Gly Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Ile
            340                 345                 350

ctg caa tgc cag ggc ttc tat cag ctg tgt ggt gtc cac cag gaa gat   1162
Leu Gln Cys Gln Gly Phe Tyr Gln Leu Cys Gly Val His Gln Glu Asp
        355                 360                 365

gtg atc tac ctc gcc ctc cca ctc tac cac atg tcc ggt tcc ctg ctg   1210
Val Ile Tyr Leu Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu
    370                 375                 380

ggc atc gtg ggc tgc atg ggc att ggg gcc aca gtg gtg ctg aaa tcc   1258
Gly Ile Val Gly Cys Met Gly Ile Gly Ala Thr Val Val Leu Lys Ser
385                 390                 395                 400

aag ttc tcg gct ggt cag ttc tgg gaa gat tgc cag cag cac agg gtg   1306
Lys Phe Ser Ala Gly Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val
                405                 410                 415

acg gtg ttc cag tac att ggg gag ctg tgc cga tac ctt gtc aac cag   1354
Thr Val Phe Gln Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln
            420                 425                 430
```

```
ccc ccg agc aag gca gaa cgt ggc cat aag gtc cgg ctg gca gtg ggc   1402
Pro Pro Ser Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly
        435                 440                 445

agc ggg ctg cgc cca gat acc tgg gag cgt ttt gtg cgg cgc ttc ggg   1450
Ser Gly Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly
    450                 455                 460

ccc ctg cag gtg ctg gag aca tat gga ctg aca gag ggc aac gtg gcc   1498
Pro Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
465                 470                 475                 480

acc atc aac tac aca gga cag cgg ggc gct gtg ggg cgt gct tcc tgg   1546
Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser Trp
                485                 490                 495

ctt tac aag cat atc ttc ccc ttc tcc ttg att cgc tat gat gtc acc   1594
Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Thr
            500                 505                 510

aca gga gag cca att cgg gac ccc cag ggg cac tgt atg gcc aca tct   1642
Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met Ala Thr Ser
        515                 520                 525

cca ggt gag cca ggg ctg ctg gtg gcc ccg gta agc cag cag tcc cca   1690
Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro
    530                 535                 540

ttc ctg ggc tat gct ggc ggg cca gag ctg gcc cag ggg aag ttg cta   1738
Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala Gln Gly Lys Leu Leu
545                 550                 555                 560

aag gat gtc ttc cgg cct ggg gat gtt ttc ttc aac act ggg gac ctg   1786
Lys Asp Val Phe Arg Pro Gly Asp Val Phe Phe Asn Thr Gly Asp Leu
                565                 570                 575

ctg gtc tgc gat gac caa ggt ttt ctc cgc ttc cat gat cgt act gga   1834
Leu Val Cys Asp Asp Gln Gly Phe Leu Arg Phe His Asp Arg Thr Gly
            580                 585                 590

gac acc ttc agg tgg aag ggg gag aat gtg gcc aca acc gag gtg gca   1882
Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala
        595                 600                 605

gag gtc ttc gag gcc cta gat ttt ctt cag gag gtg aac gtc tat gga   1930
Glu Val Phe Glu Ala Leu Asp Phe Leu Gln Glu Val Asn Val Tyr Gly
    610                 615                 620
```

```
gtc act gtg cca ggg cat gaa ggc agg gct gga atg gca gcc cta gtt   1978
Val Thr Val Pro Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Val
625                 630                 635                 640

ctg cgt ccc ccc cac gct ttg gac ctt atg cag ctc tac acc cac gtg   2026
Leu Arg Pro Pro His Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val
                645                 650                 655

tct gag aac ttg cca cct tat gcc cgg ccc cga ttc ctc agg ctc cag   2074
Ser Glu Asn Leu Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln
            660                 665                 670

gag tct ttg gcc acc aca gag acc ttc aaa cag cag aaa gtt cgg atg   2122
Glu Ser Leu Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met
        675                 680                 685

gca aat gag ggc ttc gac ccc agc acc ctg tct gac cca ctg tac gtt   2170
Ala Asn Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val
    690                 695                 700

ctg gac cag gct gta ggt gcc tac ctg ccc ctc aca act gcc cgg tac   2218
Leu Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr
705                 710                 715                 720

agc gcc ctc ctg gca gga aac ctt cga atc tgagaacttc cacacctgag     2268
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
                725                 730

gcacctgaga gaggaactct gtggggtggg ggccgttgca ggtgtactgg gctgtcaggg 2328

atcttttcta taccagaact gcggtcacta ttttgtaata aatgtggctg gagctgatcc 2388

agctgtctct gacctac                                                2405
```

<210> 2
<211> 730
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser Gln
  1               5                  10                  15

Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly Met Phe
            20                  25                  30
```

Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala Gly Ser Met
35 40 45

Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu Pro Leu Leu Leu
50 55 60

Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp Leu Pro Ala Asp Leu
65 70 75 80

Ala Phe Ala Val Arg Ala Leu Cys Cys Lys Arg Ala Leu Arg Ala Arg
85 90 95

Ala Leu Ala Ala Ala Ala Ala Asp Pro Glu Gly Pro Glu Gly Gly Cys
100 105 110

Ser Leu Ala Trp Arg Leu Ala Glu Leu Ala Gln Gln Arg Ala Ala His
115 120 125

Thr Phe Leu Ile His Gly Ser Arg Arg Phe Ser Tyr Ser Glu Ala Glu
130 135 140

Arg Glu Ser Asn Arg Ala Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp
145 150 155 160

Asp Trp Gly Pro Asp Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu
165 170 175

Gly Glu Arg Ala Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly
180 185 190

Ala Glu Phe Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala
195 200 205

Ala Pro Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly
210 215 220

Pro Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg
225 230 235 240

Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His Cys
245 250 255

Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu Phe Leu
260 265 270

Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met Gly Leu His
275 280 285

Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly Ile Ser Asp Leu
290 295 300

Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro Val Pro Gly Tyr Leu
305 310 315 320

Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys Leu Tyr Ile Phe Thr Ser
325 330 335

Gly Thr Thr Gly Leu Pro Lys Ala Ala Arg Ile Ser His Leu Lys Ile
340 345 350

Leu Gln Cys Gln Gly Phe Tyr Gln Leu Cys Gly Val His Gln Glu Asp
355 360 365

Val Ile Tyr Leu Ala Leu Pro Leu Tyr His Met Ser Gly Ser Leu Leu
370 375 380

Gly Ile Val Gly Cys Met Gly Ile Gly Ala Thr Val Val Leu Lys Ser
385 390 395 400

Lys Phe Ser Ala Gly Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val
405 410 415

Thr Val Phe Gln Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln
420 425 430

Pro Pro Ser Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly
435 440 445

Ser Gly Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly
450 455 460

Pro Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala
465 470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser Trp
485 490 495

Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp Val Thr
500 505 510

Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met Ala Thr Ser
515 520 525

Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser Gln Gln Ser Pro
530 535 540

Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala Gln Gly Lys Leu Leu
545 550 555 560

Lys Asp Val Phe Arg Pro Gly Asp Val Phe Phe Asn Thr Gly Asp Leu
565 570 575

Leu Val Cys Asp Asp Gln Gly Phe Leu Arg Phe His Asp Arg Thr Gly
580 585 590

Asp Thr Phe Arg Trp Lys Gly Glu Asn Val Ala Thr Thr Glu Val Ala
595 600 605

Glu Val Phe Glu Ala Leu Asp Phe Leu Gln Glu Val Asn Val Tyr Gly
610 615 620

Val Thr Val Pro Gly His Glu Gly Arg Ala Gly Met Ala Ala Leu Val
625 630 635 640

Leu Arg Pro Pro His Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val
645 650 655

Ser Glu Asn Leu Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln
660 665 670

Glu Ser Leu Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met
675 680 685

Ala Asn Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val
690 695 700

Leu Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr
705 710 715 720

Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile
725 730

<210> 3
<211> 30
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially Synthesized Oligo-cap Linker

<400> 3
agcaucgagu cggccuuguu ggccuacugg 30

<210> 4
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially Synthesized Primer Sequence

<400> 4
gcggctgaag acggcctatg tggccttttt ttttttttt tt 42

<210> 5
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially Synthesized Primer Sequence

<400> 5
agcatcgagt cggccttgtt g 21

<210> 6
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially Synthesized Primer Sequence

<400> 6
gcggctgaag acggcctatg t 21

<210> 7
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially

Synthesized Primer Sequence

<400> 7
ggaattccgt ggagtggtgg gggcctgggt gggaat 36

<210> 8
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially Synthesized Primer Sequence

<400> 8
cgggatccca cctgcaacgg cccccacccc acagagttc 39

<210> 9
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially Synthesized Primer Sequence

<400> 9
ggaattccgt ggagtggtgg gggcctgggt gggaat 36

<210> 10
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially Synthesized Primer Sequence

<400> 10
cgggatccga ttcgaaggtt tcctgccag 29

<210> 11
<211> 20
<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 11
aacagggctg cacgcgcctt 20

<210> 12
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

<400> 12
cgggatccca cctgcaacgg cccccacccc acagagttc 39

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP00/04549

A. CLASSIFICATION OF SUBJECT MATTER
Int.Cl[7] C12N15/12, 5/10, 1/15, 1/19, 1/21, C12P21/02
C07K14/47, 16/18, C12Q1/02, 1/68
C12P21/02,
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
Int.Cl[7] C12N15/00-15/90

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
GENBANK/DDBJ/EMBL/GENESEQ
SWISSPROT/PIR/GENESEQ
BIOSIS/MEDLINE/WPI(STN)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	WO, 99-46281, A2 (GENENTECH INC.), 16 September, 1999 (16.09.99), Full text (Family: none)	1-16
P,X	WO, 99-36537, A2 (MILLENNIUM PHARM INC.), 22 July, 1999 (22.07.99), Full text & AU, 9923108, A	1-16
X	Biochimica et Biophysica Acta, 1443, 1998 Barbara A. Fitscher et al., "Tissue distribution and cDNA cloning of a human fatty acid transport protein(hsFATP4)", p.381-385	1-16
X	Proc. Natl. Acad. Sci. USA, 95, July 1998 David Hirsch et al., "A family of fatty acid transporters conserved from mycobacterium to man", p.8625-8629	1-16
A	Cell, 79, Nov.1994 Jean E. Schaffer et al., "Expression cloning and characterization of a novel adipocyte long chain fatty	1-16

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier document but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
03 October, 2000 (03.10.00)	24 October, 2000 (24.10.00)
Name and mailing address of the ISA/ Japanese Patent Office	Authorized officer
Facsimile No.	Telephone No.

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/JP00/04549

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
	acid transport protein",p.427-436	
A	J. Biol. Chem., 271(48), Nov.1996 A. Uchiyama et al., "Molecular cloning of cDNA encoding rat very long-chain acyl-CoA synthetase", p.30360-30365	1-16
A	Circulation, 96(8)suppl., 1997 Jean E. Schaffer et al., "Cloning and structure-function analysis of human heart fatty acid transport protein", p. I363	1-16

国際調査報告

国際出願番号　PCT／JP00／04549

A.　発明の属する分野の分類（国際特許分類（IPC））

Int. Cl⁷　C12N15／12, 5／10, 1／15, 1／19, 1／21, C12P21／02
C07K14／47, 16／18, C12Q1／02, 1／68

B.　調査を行った分野

調査を行った最小限資料（国際特許分類（IPC））

Int. Cl⁷　C12N15／00－15／90

最小限資料以外の資料で調査を行った分野に含まれるもの

国際調査で使用した電子データベース（データベースの名称、調査に使用した用語）
GENBANK／DDBJ／EMBL／GENESEQ
SWISSPROT／PIR／GENESEQ
BIOSIS／MEDLINE／WPI（STN）

C.　関連すると認められる文献

引用文献のカテゴリー＊	引用文献名　及び一部の箇所が関連するときは、その関連する箇所の表示	関連する請求の範囲の番号
P, X	WO, 99－46281, A2 (GENENTECH INC.) 16. 9月. 1999 (16. 09. 99) 全文 (ファミリーなし)	1－16

☒ C欄の続きにも文献が列挙されている。　☐ パテントファミリーに関する別紙を参照。

＊　引用文献のカテゴリー
「A」特に関連のある文献ではなく、一般的技術水準を示すもの
「E」国際出願日前の出願または特許であるが、国際出願日以後に公表されたもの
「L」優先権主張に疑義を提起する文献又は他の文献の発行日若しくは他の特別な理由を確立するために引用する文献（理由を付す）
「O」口頭による開示、使用、展示等に言及する文献
「P」国際出願日前で、かつ優先権の主張の基礎となる出願の日の後に公表された文献
「T」国際出願日又は優先日後に公表された文献であって出願と矛盾するものではなく、発明の原理又は理論の理解のために引用するもの
「X」特に関連のある文献であって、当該文献のみで発明の新規性又は進歩性がないと考えられるもの
「Y」特に関連のある文献であって、当該文献と他の1以上の文献との、当業者にとって自明である組合せによって進歩性がないと考えられるもの
「&」同一パテントファミリー文献

国際調査を完了した日	国際調査報告の発送日
03. 10. 00	24.10.00

国際調査機関の名称及びあて先	特許庁審査官（権限のある職員）	4B	9838
日本国特許庁（ISA／JP） 郵便番号100－8915 東京都千代田区霞が関三丁目4番3号	鈴木　恵理子 電話番号　03－3581－1101　内線　3448		

様式PCT／ISA／210（第2ページ）（1998年7月）

C（続き）．　関連すると認められる文献

引用文献のカテゴリー＊	引用文献名　及び一部の箇所が関連するときは、その関連する箇所の表示	関連する請求の範囲の番号
P, X	WO, 99－36537, A2 (MILLENNIUM PHARM INC.) 22. 7月. 1999 (22. 07. 99) 全文 & AU, 9923108, A	1－16
X	Biochimica et Biophysica Acta, 1443, 1998 Barbara A. Fitscher et al., "Tissue distribution and cDNA cloning of a human fatty acid transport protein(hsFATP4)", p. 381-385	1－16
X	Proc. Natl. Acad. Sci. USA, 95, July 1998 David Hirsch et al., "A family of fatty acid transporters conserved from mycobacterium to man", p. 8625-8629	1－16
A	Cell, 79, Nov. 1994 Jean E. Schaffer et al., "Expression cloning and characterization of a novel adipocyte long chain fatty acid transport protein", p. 427-436	1－16
A	J. Biol. Chem., 271(48), Nov. 1996 A. Uchiyama et al., "Molecular cloning of cDNA encoding rat very long-chain acyl-CoA synthetase", p. 30360-30365	1－16
A	Circulation, 96(8) suppl., 1997 Jean E. Schaffer et al., "Cloning and structure-function analysis of human heart fatty acid transport protein", p. I363	1－16